IN THE SPECIFICATION:

On Page 5, please amend the second paragraph to read as follows:

FIG 3. Peptides 7 and 18 are Homologous to the Somatomedin B Domain of Vitronectin. The sequence of vitronectin (SEQ ID No:9) from residues 1-47 including the somatomedin B domain and RGD motif is compared with the sequences of clones 7 (SEQ ID NO:10) and 18 (SEQ ID NO:11). Homologous residues at positions 22-28 in vitronectin and in the bacteriophage derived peptides are in bold as in the RGD sequence in vitronectin.

On Page 5, please amend the third paragraph to read as follows:

FIG 4. Alanine Replacement of Peptide 7 Affects Both Bacteriophage and Vitronectin Binding to UPAR. Synthetic peptides at 40 μm were tested as competitors for binding of bacteriophage 7 (portion of SEQ ID NO:10) to biotinylated suPAR as described in Materials and Methods and shown in panel A. Bacteriophage were detected with a rabbit anti-M13 antibody as described. The indicated values are the mean of triplicate determinations. The same peptides were tested in triplicate at 50 μm in the uPA1-48:uPAR:vitronectin binding ELISA.

On Page 5, please amend the fifth paragraph to read as follows:

FIG 6: Table. The table of FIG 6 depicts the sequences (SEQ ID NOS:12-17), phage yields, and IC50s in uPAR binding assays for selected phage peptides. Legend: 1. Individual phage were incubated with biotinylated suPAR with and without 10μM uPA1-48 on streptavidin coated wells as described herein. The background yields of all phage without SuPAR in the wells ranged from 0.002-0.025%. Errors in yield are in the range 50%. 2. Apparent inhibition constant of the synthetic peptide in the uPAR receptor binding assay; errors are in the range of 20%. 3. NT = not determined because of peptide insolubility. 4. Clone 20 and 13-32 peptides were as described previously.

On Page 14, first paragraph, please amend as follows:

The invention also includes specific peptides that represent examples of a uPAR:integrin site, such as peptide 25 (SEQ ID NO:4). Clone 25 represents a distinct sequence motif, and based on the equivalent binding to D 23, identify a unique binding sufficient for inhibiting the binding pair interaction between uPAR and integrin is GYZY, where Z is M or V. Peptide 25 has been shown to bind to the urokinase receptor and modulates integrin function. The sequence of peptide 25 is (SEQ ID NO:15) AESTYHHLSLGYMYTLN, where, by alanine replacement the amino acids (SEQ ID NO:5) YHXLXXGYMYT, where X is any amino acid were determined to be important for inhibiting uPAR binding to integrin.

Pages 36-37, Example 1, last paragraph, please amend as follows:

Soluble recombinant human urokinase receptor (suPAR) was expressed and secreted from baculovirus-infected Sf9 insect cells, as described in *Goodson et al.*,

Proc.Natl.Acad.Sci.USA 91:7129-7133 (1994). The EGF-like domain of human urokinase (uPA residues 1-48) was expressed from recombinant yeast as described *Stratton-Thomas et al., Prot.Eng. 8:* 463-470 (1995). UPA1-48 was purified by a revision of the published procedure, involving ion exchange chromatography and reverse phase HPLC under reducing conditions, followed by a refolding step and rechromatography on reversed phase HPLC of the oxidized material. Soluble uPAR was purified on a column of immobilized uPA1-48, eluted at low pH, biotinylated according to *Kaufman et al. Anal.Biochem.211:*261-266 (1993) and purified on a Soft-Avidin column (Promega Corporation, Madison, WI). The uPAR fragment encompassing domains 2 and 3 (amino acids 93-313) with a C-terminal epitope tag of E-Y-M-P-M-E (SEQ ID NO:18) as described in *Grussenmeyer et al. Proc.Natl.Acad.Sci.USA 82:* 7952-7954 (1985) was expressed in baculovirus infected Sf9 insect cells, and purified from the conditioned media by affinity chromatography on an anti-epitope antibody column. Peptides were synthesized at Chiron Mimotopes (Melbourne, Australia) with fee amino termini and amidated carboxyl termini, and were greater than 70% pure by HPLC and MS analysis. A variant of clone 20 peptide was prepared with the sequence: AE PMPHSLNFSQYAWYT (SEQ ID NO:7). A scrambled version of clone 7 had the sequence: VEYRDAYSYPQYLSYLE (SEQ ID NO:8). Recombinant PAI-1 was obtained from American Diagnostica. Horse-radish peroxidase (HRP) conjugated streptavidin was from Pierce Chemical, Rockford, IL. Anti-M13 antibody was from Pharmacia, Piscataway, NJ.

Page 39, last paragraph, please amend as follows:

It was also shown by the inventors that bacteriophage bound to sUPAR domain 2-3 fragment. Protein G, 100 μl, 1 mg/ml in 50 mM Na_2CO_3, pH9.6, was added to MaxiSorp wells, incubated overnight at 4°C and then washed with PBS/BSA. Fifty μl of monoclonal antibody to the epitope tag EYMPME (SEQ ID NO: 18) was added at 1 mg/ml in PBS/BSA and incubated for 2 hours at room temperature. The wells were washed, recombinant sUPAR domain 2-3 (1.7 μM in PBS/BSA) was added and incubated for 1.5 hours at room temperature. The wells were washed prior to the addition of bacteriophage (approximately 10^8 pfu), and then treated as described in the previous section for binding to suPAR.

Page 41, last paragraph bridging to page 42, please amend as follows:

It was also then determined that the bacteriophage peptides are homologous to the somatomedin B domain of vitronectin, which is also the binding site of PAI-1. The sequences of bacteriophage derived peptides 7 and 18 were examined for homology to this domain. As shown in FIG 3, there is a conserved motif, LXXArY (where X is a hydrophilic residue, and AR = F,Y) between residues 24-28 of the somatomedin B domain and clone 7 and 18 peptides. In addition, clones 7 and 18 share the sequence E-L-d just N-terminal to the conserved leucine, whereas the related sequence D-E-L is found in the somatomedin B domain of vitronectin at residues 22-24, adjacent to the conserved sequence LCSYY (SEQ ID NO: 9).